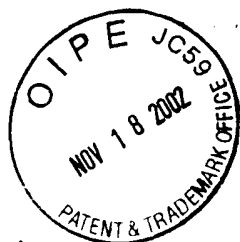




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eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu  
81 GTCTCCAAAA ACAGTAGCCA AGACAAAAAT GGAAAGGGAG  
ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG  
121 GAGTAATAAT CCGAAAGAG AAGTTCTGGA AGCCACCCAG  
lyValIleIle ProLysGlu LysPheTrpLys ProProSe  
161 CACTCCCCCG GCATCTGGA ACAGGGAACA GGAGAAGCTG  
rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu  
201 AACAGGIGGT ACAATCCCAT CTGGAACAGG GTGGCCAATC  
AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG  
241 AGACAGGGGA GCTAGCCACA TCTCCAAACA CAAGTCACT  
InThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe  
281 GAGCTATTGT GAACAGACT CGACGGTCAT GACAGCTGTG  
uSerTyrCys GluProAspSer ThrValMET ThrAlaVal  
321 ACAGATTTTA ATAATCTGCC GGACAGATTT AAAGACTTTC  
ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL  
361 TCTTGATTTT GAGATGCGCG AATTACTGCG TGCTTATAGA  
euLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs  
401 TCAACCGAAG AAATGTGCAA AGAAGCCCTT CTACTATTG  
pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu  
441 GCGATAAAGT CCTCATTC ACATTTTGCC AGAAGGCAAG  
AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA  
481 CAATTGGGA GTCTTGGGCG CGAGAAACA ACGTAGGGAA  
laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs  
521 CCAGACAGTA GTGAGGGTCT TCTGTGTCGG CAAGACACCC  
nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro  
561 CCAGAGGACA ACCACCTGA CCTTTGGGAC ATGCTTAAGT  
ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP  
601 TTGAGAGTGA CAAGCACCAG GACATCTCA TGTTGGAATA  
heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTyr  
641 TAGAGACACA TTCTTCAACC TGTCCTGAA GGAAGTGTG  
rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1A



681 TTTCCTAGGT GGGTGAGCAC TTCTGTCCA GAAGCAGAGT  
PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP  
721 TTGICTTCAA GGGCGATGAT GAAGIGTTTG TGAACACCCA  
heValPheLys GlyAspAsp AspValPheVal AsnThrHi  
761 TCACATCCTT AATTACTTGA ATAGCTTATC CAAGAGCAAA  
sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys  
801 GCCAAGACT TGTTCTATAGG TGAAGIGATC CACAATGCTG  
AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG  
841 GGCTCACCG GGATAAGAAA CTGAAGTACT ACATCCAGA  
lyProHisArg AspLysLys LeuLysTyrTyr IleProGl  
881 AGTCTTCTAC ACGGGGTCTT ACGCACCGTA TCGCGGGGT  
uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly  
921 GGTGGATTCC TGTACTCCCG CCCCCTTGGC TTGAGGCTGT  
GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT  
961 ACAGTGGGAC TAGCGGGGTC CATCTCTACC CTATTGATGA  
yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs  
1001 TGTTTATACG GGAATGTGCC TTCAGAAACT GGGCCTTGTT  
pValTyrThr GlyMETCysLeu GlnLysLeu GlyLeuVal  
1041 CCAGAGAAGC ACAAAGGCTT CAGGACATTT GATATTGAAG  
ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG  
1081 AGAAAAATAA GAAAAATATT TGTTCCTATA TAGAATAAT  
luLysAsnLys LysAsnIle CysSerTyrIle AspLeuME  
1121 GTTAGTACAT AGCAGAAAAC CTCAAGAGAT GATTGATATC  
TLeuValHis SerArgLysPro GlnGluMET IleAspIle  
1161 TGGTCTCAGT TGCAAAGTCC TAATTTAAAA TGCTGA  
TrpSerGlnLeu GlnSerPro AsnLeuLys Cys

FIG. 1B

MAX - R R K V - - - - - L L R - L L - - - V

10 20 30

M S V G - - - R - - - - - K L  
M A - - - S - - - S C - - - Y - - - V  
M A P - - - - - - - - - A V L T A L P N R M S - - - S - - - K W S L  
M Q S K H R F L - - - - - - - - - C - - - L - - - V  
M L Q W R F R H C C F A K M T W N A K R S I F - - - T H - - - I G V

L S L V X L X X X F X F L X H - - - W - - - - - - - - -

40 50 60

L G I L M M A N V - - I Y - - - I V E V S K N S S Q D K N G K G G  
L S V V C - - - - - - - - - A S A - - - - - - - - -  
L - - - - - L S L L S - - - V - - - - - - - - -  
L P L I L L V D Y C G L - - - T H L H - - - - - - - - -  
L S L V F L F A M F L F F N H D - - - L P G R A G F K E N P V

- - - F - - - F - - - P - - - - - - - - - - - - - I W Y

70 80 90

V I I P K E K - - W K - - - P S T P R A Y W N R E Q E K L N R W Y  
- L W Y  
- W Y  
E L N F E R H - - H Y - - - - - - - - - - - - - - -  
T Y T F R G - - - R S T K S E T N H S S L R - - - - - N I W K

L S I P - - - L R P Q T G S X S X S X X L S H L - Y - - - - N

100 110 120

N P I L N R V A N - - T E L A T E P N T S H L S Y C E P D S  
L S I T - - - - - S - - - Y T G - - - K P F S H I - - - - -  
L S L P H Y -  
- - - - - L N D D - - - G S A S G L D K F A Y - - - - -  
E T V F Q T L R E P O T A T N S N N T D L S P Q G V T G L E N

T V X R X N X X F N N X X T R - - - - - P I N S X X F E F

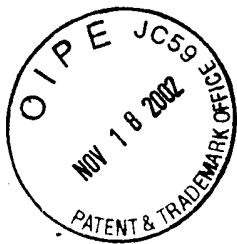
130 140 150

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T V A R K N F T F G M I R P P - - - - - P I N P H S F F F  
V I E P V W M Y F - Y E Y E - - - - - P I Y R Q D F R F  
- - - - - - - - - - - - - - - - L R V P S F T A F V  
T L S A N G S I Y R E K G T G - - - - - H P N S Y H - - - K Y

L I D E P X K C X K K - P F L V L L I K S X P G X F X A R Q

160 170 180

FIG. 2A



160 170 180  
L I P Q F K A H - P L A L I P H A R A  
L I N E F N E N I I S T H K E D A R  
T L R H S N S H Q N I V T R S D V K A R  
P V Q A R - - - - - T M A V N S R R E E  
I N F E Q E S I A A E Q I E N R  
A I R E T W G X E X N F X G I X V X R V F L L G K X A - E X  
190 200 210  
A I R E S W G R E T N V G N O T V V F L L G F T P P E D  
A I R E T W G D E N H F K G K I A T L F L L G F N A - - -  
A I P V T W G E K K S W W G Y E V L T F F L L G Q Q A - E R  
A I P R T W G Y E G R E S D V H L R E V F L L G T A E D S E  
A I P Q T W G N F S L A P G Q I T E I F L L G L S I - - K  
X D P X L X X M V E X E S R X H G D I I Q Q D F L D T Y F N  
220 230 240  
N H F D L S D M L K F E S D K Q D I L M W N Y R D T F F E  
- D F V L N Q M V E Q E S Q I F H D I I V E D F I C S H H  
E D K T A L S L E D E H V L Y J D I I R D D F L D T Y N N  
K - - - - - V A W E S H E H G D I L A D F T D A Y E N  
L N G Y I Q R A I L E E S F Q Y H D I I Q C E Y L D T Y Y  
L T L K T L M G M R W V A T F C P X A E Y V M K T D S D V F  
250 260 270  
S L K E V L F L R W V S I S C I D A F F F K G D D D V F  
L T L K T L M G M R W V A T F C S K A K Y V M K T D S D V F  
L T L K T I M A F R W V M E F C I N A K Y I M K T D T D V F  
N T L K T M L G M R W A S E Q F N R S F Y L F V L D E Y Y  
L T I K T L M G M N W V A T Y C I H I P Y V M K T D S D M E  
V N T X N L L N K L L K P S L S H R X X L F T G Y - V I X G  
280 290 300  
N N T H H I L N Y L N S L S K K A K D F I C - D V I H N  
N M D N L I Y L L F F S T K P R R Y F T G Y - V I N  
I N T G N I V K Y L I - - N N S E K F F T G Y P L I D N  
S A K N V L K F L G R G R O Q P E L F A G H V F Q T  
N N T E Y L I N F L L R D P P H N Y F T G Y - L M R

FIG. 2B



YGPXRDKFSKWIYPXDLYPF XVYPPYCSGG  
310 320 330  
AGFHRDRLKLYEVEFTGPPVAGSG  
-GEIRVRMRYDSNPIFCSCT  
YS-YFGFHHNHSYQEYPKFPFYCSGL  
-SELFFHKFSKWIYVSLEEYPERDRWPPYVTA  
YAFNNFNDSKWIYMPPLYEYSERYEYVF  
GYIFSGDLAERLYKASLHVRLLLHLEDVYVG  
340 350 360  
FLYSCPLALVYSATSRHYPIDDVYT  
GYIFSAADVLIETEDVYV  
GYIMSGDIVPVEMMSKPIKFEDVYV  
AFLLQKALRQAVLPRFRFDVYL  
LYVESGDLKIFVGIREDVYV  
ICLXKLGIDPXXPXG---FNHW-KXXKSXC  
370 380 390  
MCLQKLGVLVEKHKGFRTFDIEEKNKKNIC  
LCLRKLGLGHFQNSG---FNHW-FMAYELC  
ICINLIKVIHIEEDTNLFFLY-RIHLDV  
IVALHAGISLQHCDD---FRFHRPAYGPD  
CIAKILRIDEVPPNEFVFNHW-RVSYSS  
SYSRVIAVHQF-SPEEMIRIWNXL-Q-KNL  
400 410 420  
YIDLMLVHSR-KQEMIDISQI-SP  
RYRRVITVHCICPEEMHPIWIDMSSSKH  
QLRPIVIAAHGF-SKEITFQVML--RT  
YSSVIAASHGDEEMTVWKE-----  
KYSHLITSHGE-QESPLIKYNNHQNNHN  
XC-----Y-----  
430  
KC.  
RC.  
TC-----HY  
-C-----RSANY-----A  
ACANAAKEKAGRVRHRKLH

FIG. 2C

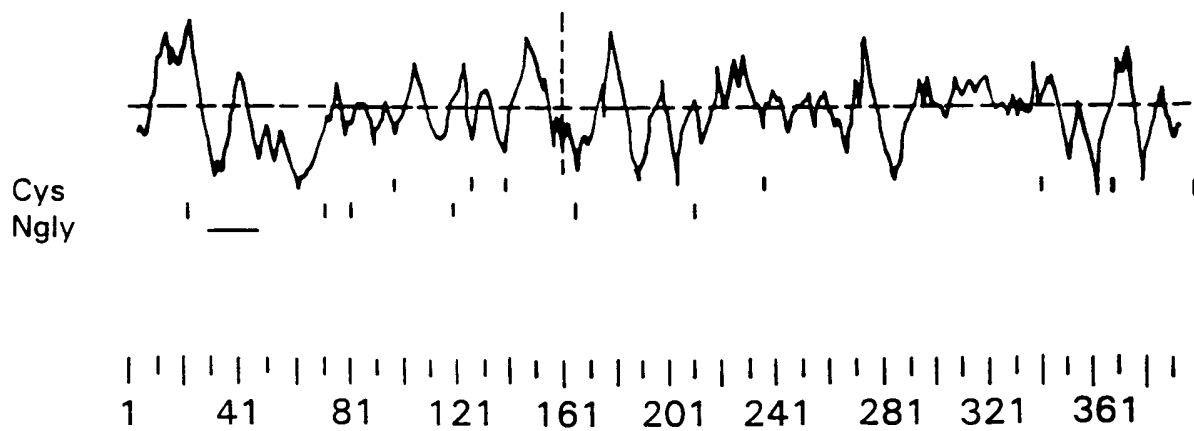


FIG. 3

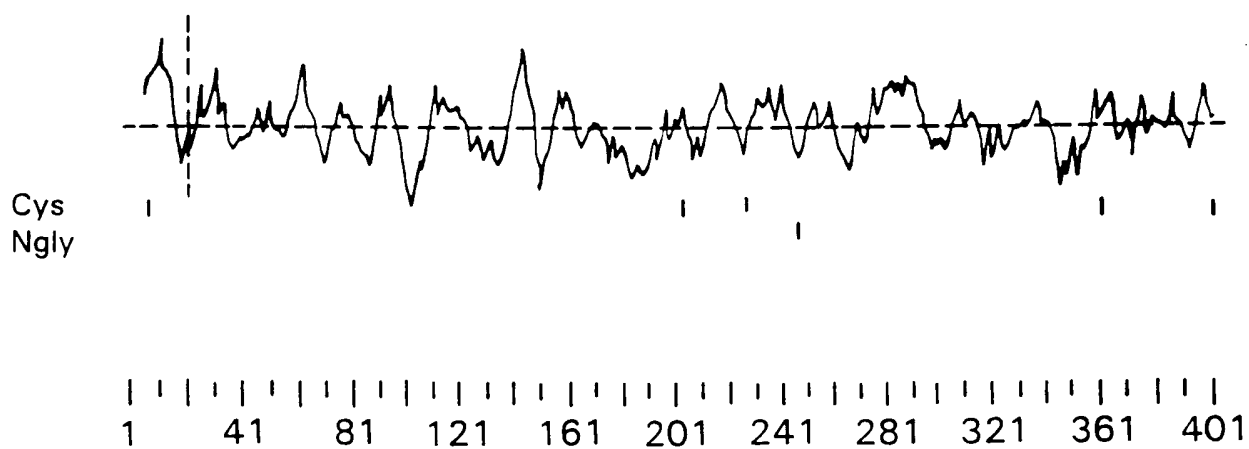
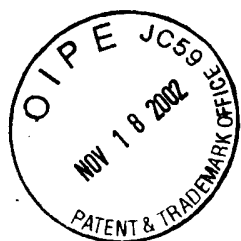
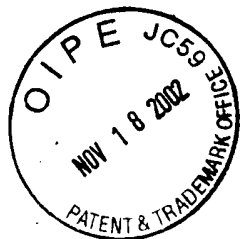


FIG. 5



1 ATGATTIGOC CTCAGCTTT ACTGGTTATT TTAAGAAATT  
METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL  
41 TAATAACGGGA AGAAAAATC ATTTCTCAAG AGATCCTCAA  
euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs  
81 TTTGATTGAA TTAAGGATGA AAAAAGGGAA TATTCAGTTG  
nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu  
121 ACAAACTCTG CAATCAGTGA TGCATTAAAA GAAATCGATA  
ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS  
161 GTAGTGTGCT CAATGTTCCT GTCAACGGGG AGACGGGATC  
erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe  
201 AGGGAAGTCC AGCTTCATCA ATACCTGAG AGGCATTGGG  
rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly  
241 AATGAAGAAG AAGGTGCAGC TAAACTCGG GTGGTGGAGG  
AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV  
281 TAACCATGGA AAGACATCCA TACAAACACC CCAATATACC  
alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr  
321 CAATGIGGTT TTTTGGGACC TGCTGGGAT TGGAGGCACA  
oAsnValVal PheTrpAspLeu ProGlyIle GlySerThr  
361 AATTTCOCAC CAAACACTA CCTGGAGAAA ATGAAGTTCT  
AsnPheProPro AsnThrTyr LeuGluLys METLysPheT  
401 ATGAGTACGA TTCTTCATT ATTATTTCGG CCACAGCTT  
yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh  
441 CAAGAAAAAT GATATAGACA TTGCCAAAGC AATCAGCATG  
eLysLysAsn AspIleAspIle AlaLysAla IleSerMET  
481 ATGAAGAAGG AATTCTACTT CGTGAGAAC AAGGTGGACT  
METLysLysGlu PheTyrPhe ValArgThr LysValAspS  
521 CTGACATAAC AAATGAAGCA GATGGCAAAC CTCAAACCTT  
erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh  
561 TGACAAAGAA AAGGTCTGCT AGGACATCCG CCTTAACTGT  
eAspLysGlu LysValLeuGln AspIleArg LeuAsnCys  
601 GTGAACACCT TTAGGGAGAA TGGCATTGCT GAGCCACCAA  
ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI  
641 TCTTCTGCT CTCTAACAAA AATGTTTGTC ACTATGACTT  
lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4A



681 CCCCCTCCTG ATGGACAAGC TGATAAGTGA CCTCCCTATC  
eProValLeu METAspLysLeu IleSerAsp LeuProIle  
721 TACAGGAGAC ACAATTTTAT GGCTCCTTA CCAATATCA  
TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT  
761 CAGATTTCAGT CATTGAAAAG AAGCGGCAAT TTCTGAAGCA  
hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGI  
801 RAGGATTTGG CTGGAAGGAT TTGCTGCTGA CCTAGTGAAT  
nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn  
841 ATCATCCCTT CTCGACCTT TCTCTTGGAC AGTGATTTGG  
IleIleProSer LeuThrPhe LeuLeuAsp SerAspLeuG  
881 AGACTCTGAA GAAAGCATG AAATTCTAOC GCACTIGTGT  
luThrLeuLys LysSerMET LysPheTyrArg ThrValPh  
921 TGGAGTGGAT GAAACATCTT TGCAGAGATT AGCTAGGGAC  
eGlyValAsp GluThrSerLeu GlnArgLeu AlaArgAsp  
961 TGGGAAATAG AGGTGGATCA GGTGGAGGCC ATGATAAAAT  
TrpGluIleGlu ValAspGln ValGluAla METIleLysS  
1001 CTCCTGCTGT GTTCAAACCT ACAGATGAAG AAACAATACA  
erProAlaVal PheLysPro ThrAspGluGlu ThrIleGI  
1041 AGAAAGGCCT TCAAGATATA TTCAGGAGTT CTGTTTGGCT  
nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla  
1081 AATGGGTACT TACTTCTAA AAATAGTTTT CTAAAGAAA  
AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI  
1121 TATTTTACCT GAAATATTAT TTCTTGACA TGGTGACTGA  
lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGI  
1161 GGATGCTAAA ACTCTCTTA AAGAGATATG TTTAAGAAAC  
uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn  
1201 TAG

FIG. 4B



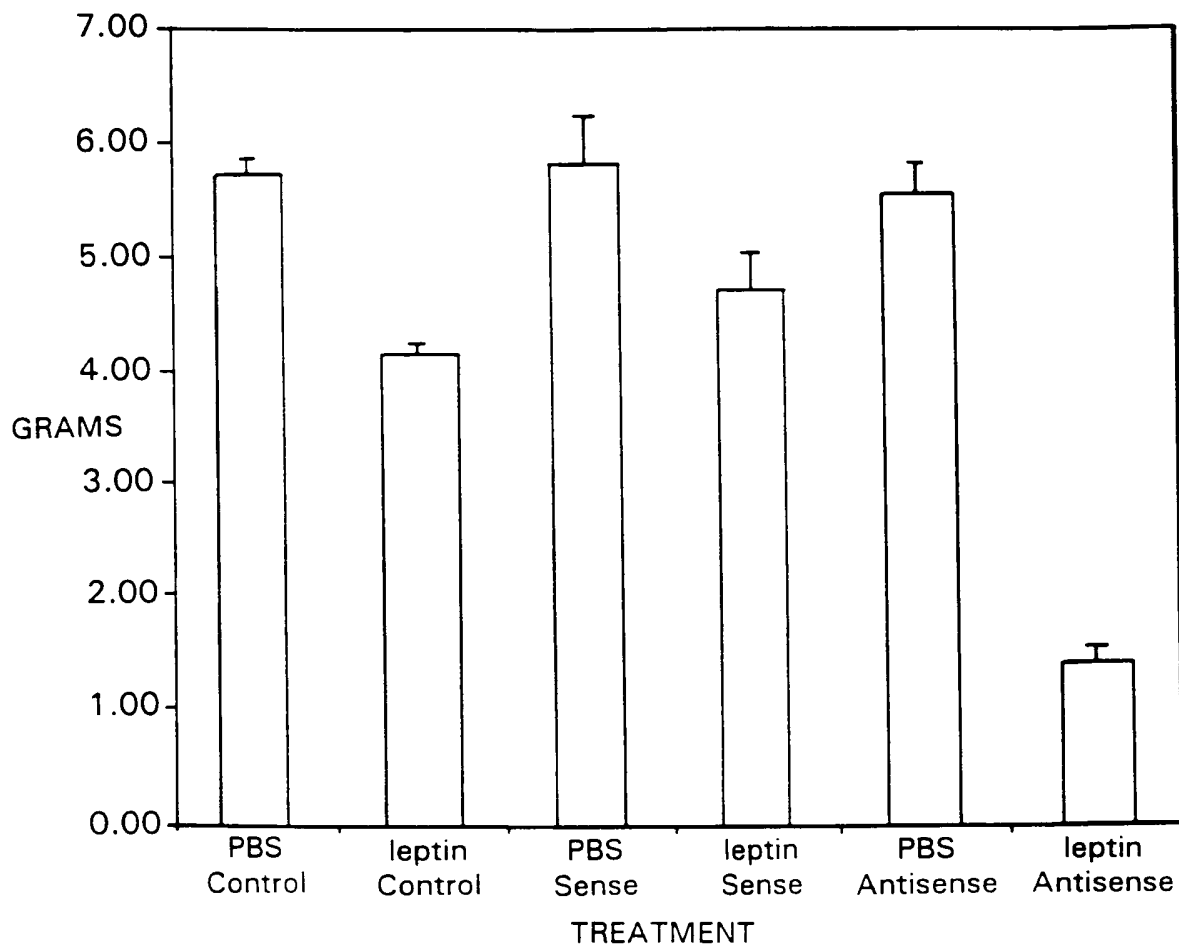
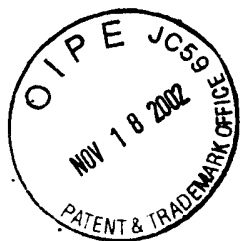
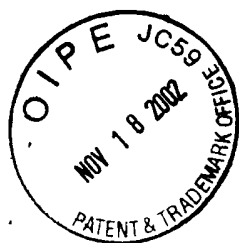


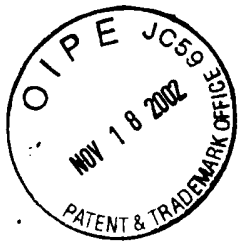
FIG. 6



5'

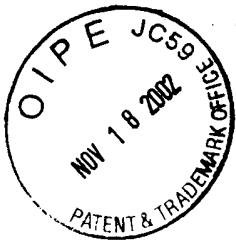
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GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC  
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTTGGA  
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA  
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG  
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG  
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT  
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG  
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCCGTGGTTACGGGT  
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG  
CAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT  
TGTTGCTGGCGATTAAAGTCCCTCACTCCACATTTTGCCAGAAGGC.AAGCAATC  
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACC.AAACGGTGGTGCGA  
GTCTTCCTGCTGGGCCAGACACCCCCAGAGGACAACC.ACCCCGACCTTTCAG  
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA  
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG  
TAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGATGACGATGTT  
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA  
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG  
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC  
ACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGG  
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATGATGACGTTTATAC  
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FIG. 7A



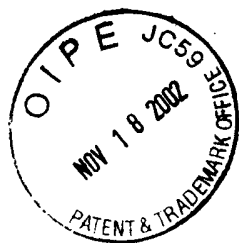
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CAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAACTCAATTTKG  
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT  
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC  
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT  
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA  
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

FIG. 7B



MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE  
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN  
NLPDRFKDFLLYLRCRNYSLLDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWG  
QESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNRYRDTFFNL  
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV  
IHNA GPHRDKKLKYYTPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY  
PIDDVYTGMCLOKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM  
IDIWSQLQSAHLKC

FIG. 8



246 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTG--GG-TATCCTGATGATGGCAAATGTC 302  
|||||  
1 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTGTTGGGTATCCTGATGATGGCAAATGTC 60

303 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 362  
|||||  
61 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 120

363 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 422  
|||||  
121 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 180

423 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 482  
|||||  
181 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 240

483 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 542  
|||||  
241 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 300

543 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 602  
|||||  
301 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 360

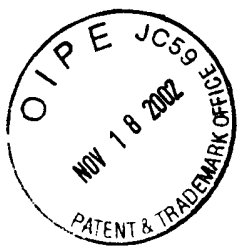
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|||||  
361 CTGCTGTATTTGAGATGCCGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCA 420

663 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 722  
|||||  
421 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 480

723 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 782  
|||||  
481 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 540

783 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCGACCTTTCAGATATGCTGAAA 842  
|||||

FIG. 9A



541 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAA 600

843 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAAC 902  
|||||

601 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAAC 660

903 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 962  
|||||

661 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 720

963 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 1022  
|||||

721 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 780

1023 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 1082  
|||||

781 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 840

1083 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 1142  
|||||

841 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 900

1143 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 1202  
|||||

901 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 960

1203 TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1262  
|||||

961 TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1020

1263 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1322  
|||||

1021 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1080

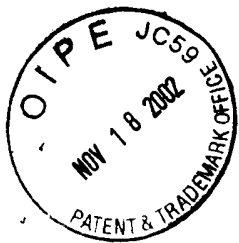
1323 GAGAAAAACAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1382  
|||||

1081 GAGAAAAACAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1140

1383 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAATGCTAA 1439  
|||||

1141 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAATGCTAA 1197

FIG. 9B



MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN  
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN  
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN

REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL  
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL  
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF  
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF  
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF

LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF  
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF  
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF

VFKGDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY  
VFKGDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY  
VFKGDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE  
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE  
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC  
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC  
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC

FIG. 10

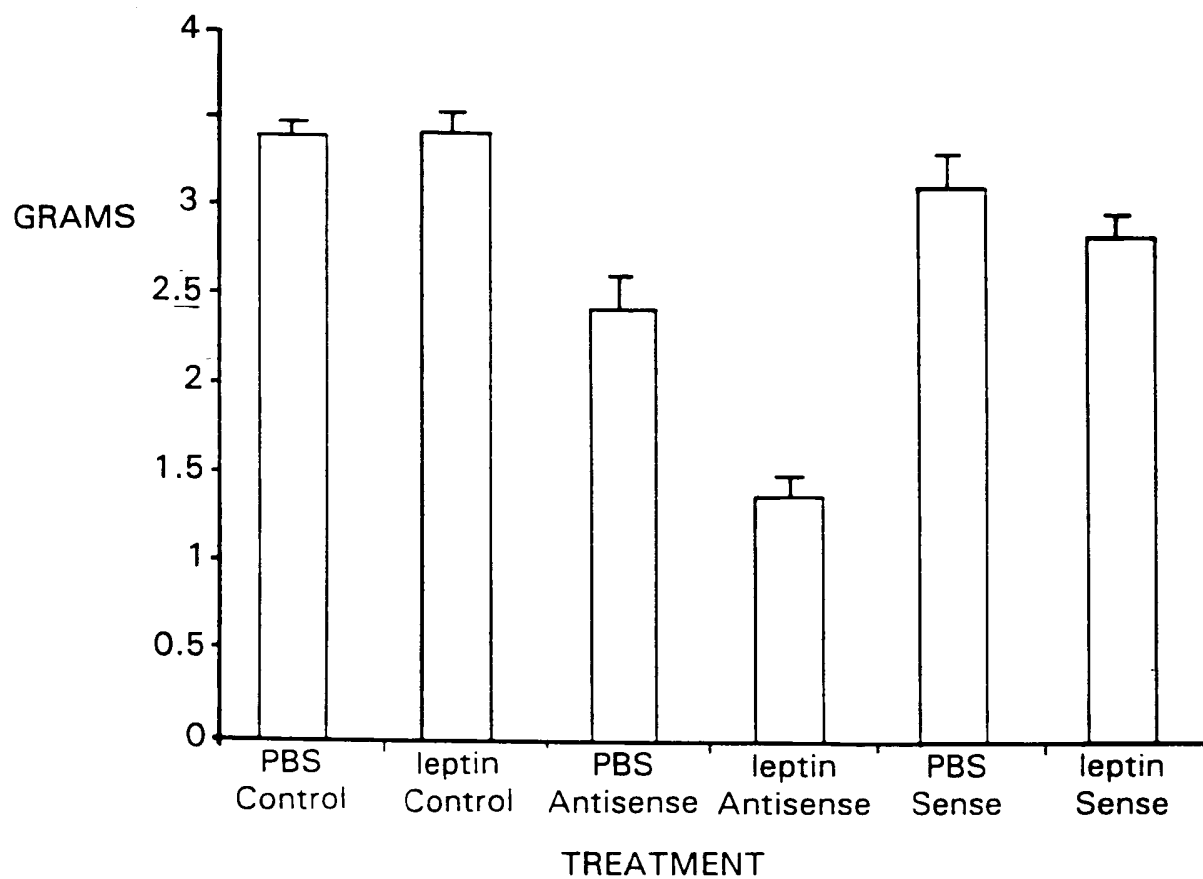
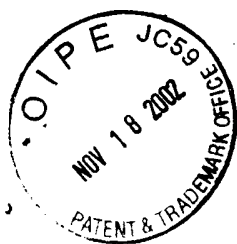


FIG. 11